- 1 -

SEQUENCE LISTING

<110> International Flower Developments Pty. Ltd.
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       Tanaka, Yoshikazu (US only)
       Mason, John (US only)

<120> Genetic Sequences and Uses Therefor

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<150> AU 2002951088
<151> 2002-08-30

<150> AU 2002952835
<151> 2002-09-16

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Leu Gly Ala Met Pro His Val Ser Leu Ala Lys Met Ala Lys Lys Tyr
    50   55   60

Gly Ala Ile Met Tyr Leu Lys Val Gly Thr Cys Gly Met Ala Val Ala
65   70   75   80

Ser Thr Pro Asp Ala Ala Lys Ala Phe Leu Lys Thr Leu Asp Ile Asn
            85   90   95

Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Asn
            100   105   110

Ala Gln Asp Met Val Phe Ala His Tyr Gly Pro Arg Trp Lys Leu Leu
        115   120   125

Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Glu Asn
    130   135   140

Trp Ala Asn Val Arg Ala Asn Glu Leu Gly His Met Leu Lys Ser Met
145   150   155   160

Ser Asp Met Ser Arg Glu Gly Gln Arg Val Val Val Ala Glu Met Leu
            165   170   175

Thr Phe Ala Met Ala Asn Met Ile Gly Gln Val Met Leu Ser Lys Arg
        180   185   190

Val Phe Val Asp Lys Gly Val Glu Val Asn Glu Phe Lys Asp Met Val
        195   200   205

Val Glu Leu Met Thr Ile Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile
    210   215   220

Pro Cys Leu Ala Trp Met Asp Leu Gln Gly Ile Glu Lys Arg Met Lys
225   230   235   240

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Arg Leu His Lys Lys Phe Asp Ala Leu Leu Thr Lys Met Phe Asp Glu
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His Lys Ala Thr Thr Tyr Glu Arg Lys Gly Lys Pro Asp Phe Leu Asp
            260         265             270

Val Val Met Glu Asn Gly Asp Asn Ser Glu Gly Glu Arg Leu Ser Thr
        275             280             285

Thr Asn Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
    290             295             300

Thr Ser Ser Ser Ala Ile Glu Trp Ala Leu Ala Glu Met Met Lys Asn
305             310             315             320

Pro Ala Ile Leu Lys Lys Ala Gln Ala Glu Met Asp Gln Val Ile Gly
            325             330             335

Arg Asn Arg Arg Leu Leu Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu
        340             345             350

Arg Ala Ile Cys Lys Glu Thr Phe Arg Lys His Pro Ser Thr Pro Leu
        355             360             365

Asn Leu Pro Arg Ile Ser Asn Glu Pro Cys Ile Val Asp Gly Tyr Tyr
    370             375             380

Ile Pro Lys Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
385             390             395             400

Asp Pro Gln Val Trp Glu Asn Pro Leu Glu Phe Asn Pro Glu Arg Phe
            405             410             415

Leu Ser Gly Arg Asn Ser Lys Ile Asp Pro Arg Gly Asn Asp Phe Glu
            420             425             430

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
        435             440             445

Gly Ile Val Met Val Glu Tyr Ile Leu Gly Thr Leu Val His Ser Phe
    450             455             460
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Asp Trp Lys Leu Pro Ser Glu Val Ile Glu Leu Asn Met Glu Glu Ala
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Thr His Ile Phe Ile Ser Thr Leu Leu Ser Ile Thr Asn Gly Arg Arg
                20                  25                  30


Leu Pro Pro Gly Pro Arg Gly Trp Pro Val Ile Gly Ala Leu Pro Leu
            35                  40                  45


Leu Gly Ala Met Pro His Val Ser Leu Ala Lys Met Ala Lys Lys Tyr
        50                  55                  60


Gly Ala Ile Met Tyr Leu Lys Val Gly Thr Cys Gly Met Val Val Ala
65                  70                  75                  80


Ser Thr Pro Asp Ala Ala Lys Ala Phe Leu Lys Thr Leu Asp Leu Asn
                85                  90                  95


Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Gly
                100                 105                 110
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Ala Gln Asp Met Val Phe Ala His Tyr Gly Pro Arg Trp Lys Leu Leu
        115             120             125

Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Glu Asn
        130             135             140

Trp Ala Asn Val Arg Ala Asn Glu Leu Gly His Met Leu Lys Ser Met
145             150             155             160

Phe Asp Met Ser Arg Glu Gly Glu Arg Val Val Val Ala Glu Met Leu
                165             170             175

Thr Phe Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Lys Arg
            180             185             190

Val Phe Val Asn Lys Gly Val Glu Val Asn Glu Phe Lys Asp Met Val
        195             200             205

Val Glu Leu Met Thr Thr Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile
        210             215             220

Pro Cys Leu Ala Trp Met Asp Leu Gln Gly Ile Glu Lys Gly Met Lys
225             230                 235             240

Arg Leu His Lys Lys Phe Asp Ala Leu Leu Thr Lys Met Phe Asp Glu
                245             250             255

His Lys Ala Thr Ser Tyr Glu Arg Lys Gly Lys Pro Asp Phe Leu Asp
            260             265             270

Cys Val Met Glu Asn Arg Asp Asn Ser Glu Gly Glu Arg Leu Ser Thr
        275             280             285

Thr Asn Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
    290             295             300

Thr Ser Ser Ser Ala Ile Glu Trp Ala Leu Ala Glu Met Met Lys Asn
305             310             315             320

Pro Ala Ile Leu Lys Lys Ala Gln Gly Glu Met Asp Gln Val Ile Gly
            325             330             335
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Arg Ala Ile Cys Lys Glu Thr Phe Arg Lys His Pro Ser Thr Pro Leu
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Asn Leu Pro Arg Ile Ser Asn Glu Pro Cys Ile Val Asp Gly Tyr Tyr
    370                 375                 380

Ile Pro Lys Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
385                 390                 395                 400

Asp Pro Glu Val Trp Glu Asn Pro Leu Glu Phe Tyr Pro Glu Arg Phe
            405                 410                 415

Leu Ser Gly Arg Asn Ser Lys Ile Asp Pro Arg Gly Asn Asp Phe Glu
            420                 425                 430

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
            435                 440                 445

Gly Ile Val Met Val Glu Tyr Ile Leu Gly Thr Leu Val His Ser Phe
    450                 455                 460

Asp Trp Lys Leu Pro Ser Glu Val Ile Glu Leu Asn Met Glu Glu Ala
465                 470                 475                 480

Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Glu Ala Met Val Thr
            485                 490                 495

Pro Arg Leu Pro Ile Asp Val Tyr Ala Pro Leu Ala
            500                 505
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actgaagctc agaaaagttt atgaaggtga gaactgagaa gggcaaggca tttggtagtt  1920
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- 10 -

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- 11 -

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- 12 -

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            20                  25                  30


Leu Pro Pro Gly Pro Ser Gly Trp Pro Leu Val Gly Ala Leu Pro Leu
        35                  40                  45


Leu Gly Ala Met Pro His Val Thr Leu Ala Asn Leu Ala Lys Lys Tyr
    50                  55                  60


Gly Pro Ile Met Tyr Leu Lys Met Gly Thr Cys Asp Met Val Val Ala
65                  70                  75                  80


Ser Thr Pro Asp Ser Ala Arg Ala Phe Leu Lys Thr Leu Asp Leu Asn
                85                  90                  95


Phe Ser Asp Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Gly
            100                 105                 110


Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly Pro Arg Trp Lys Thr Leu
            115                 120                 125


Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Asp Asp
    130                 135                 140


Trp Ala His Val Arg Ala Asn Glu Leu Gly His Met Leu Asn Ala Met
145                 150                 155                 160
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```
Cys Glu Ala Ser Arg Cys Gly Glu Pro Val Val Leu Ala Glu Met Leu
            165             170                 175

Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Arg Arg
        180             185                 190

Val Phe Val Thr Lys Gly Thr Glu Ser Asn Glu Phe Lys Asp Met Val
        195             200                 205

Val Glu Leu Met Thr Ser Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile
    210             215                 220

Pro Ser Ile Ala Trp Met Asp Leu Gln Gly Ile Glu Arg Gly Met Lys
225             230                 235                 240

Lys Leu His Thr Lys Phe Asp Val Leu Leu Thr Lys Met Met Lys Glu
            245             250                 255

His Arg Ala Thr Ser His Glu Arg Glu Gly Lys Ser Asp Phe Leu Asp
            260             265                 270

Val Leu Leu Glu Glu Cys Glu Asn Thr Asn Gly Glu Lys Leu Asn Val
    275             280                 285

Thr Asn Val Lys Ala Val Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
    290             295                 300

Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu Thr Glu Met Met Lys Asn
305             310                 315                 320

Pro Thr Ile Leu Lys Lys Thr Gln Glu Glu Met Asp Arg Val Ile Gly
            325             330                 335

Arg Asp Arg Arg Leu Leu Glu Ser Asp Val Ser Lys Leu Pro Tyr Leu
            340             345                 350

Gln Ala Ile Ala Lys Glu Thr Tyr Arg Lys His Pro Ser Thr Pro Leu
            355             360                 365

Asn Leu Pro Arg Ile Ala Ile Gln Ala Cys Glu Val Asp Gly Tyr Tyr
    370             375                 380
```

- 14 -

```
Ile Pro Lys Asp Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
385           390             395             400


Asp Pro Ser Val Trp Glu Asn Pro Ser Glu Phe Ser Pro Glu Arg Phe
              405             410             415


Leu Ser Glu Glu Asn Gly Lys Ile Ser Pro Gly Gly Asn Asp Phe Glu
              420             425             430


Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
          435             440             445


Gly Met Val Leu Val Ser Tyr Ile Leu Gly Thr Leu Val His Ser Phe
      450             455             460


Asp Trp Lys Leu Pro Asn Gly Val Ser Glu Ile Asn Met Asp Glu Ser
465             470             475             480


Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Ser Ala Thr Val Ser
              485             490             495


Pro Arg Leu Ala Pro Ser Ala Tyr Val Ile
          500             505
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<210>  11
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<212>  DNA
<213>  viola

<220>
<221>  misc_feature
<222>  (307)..(307)
<223>  n = any nucleotide


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cggttggccc ttggtgggcg ccctccctct cctaggcgcc atgcctcacg tcgcactagc   180

caaactcgct aagaagtatg gtccgatcat gcacctaaaa atgggcacgt gcgacatggt   240

ggtcgcgtcc accccgagt cggctcgagc cttcctcaaa acgctagacc tcaacttctc    300

caaccgncca cccaacgcgg gcgcatccca cctagcgtac ggcgcgcagg acttagtctt   360

cgccaagtac ggtccgaggt ggaagacttt aagaaaattg agcaacctcc acatgctagg   420
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cgggaaggcg ttggatgatt gggcaaatgt gagggtcacc gagctaggcc acatgcttaa   480

agccatgtgc gaggcgagcc ggtgcggggg gcccgtggtg ctggccgaga tgctcacgta   540

cgccatggcg aacatgatcg gtcaagtgat actcagccgg cgcgtgttcg tgaccaaagg   600

gaccgagtct aacgagttca aagacatggt ggtcgagttg atgacgtccg ccgggtactt   660

caacatcggt gacttcatac cctcgatcgc ttggatggat ttgcaaggga tcgagcgagg   720

gatgaagaag ctgcacacga agtttgatgt gttattgacg aagatggtga aggagcatag   780

agcgacgagt catgagcgca aagggaaggc agatttcctc gacgttctct tggaagaatg   840

cgacaataca aatggggaga agcttagtat taccaatatc aaagctgtcc ttttgaatct   900

attcacggcg ggcacggaca catcttcgag cataatcgaa tgggcgttaa cggagatgat   960

caagaatccg acgatcttaa aaaaggcgca agaggagatg gatcgagtca tcggtcgtga   1020

tcggaggctg ctcgaatcgg acatatcgag cctcccgtac ctacaagcca ttgctaaaga   1080

aacgtatcgc aaacaccggt cgacgcctct caacttgccg aggattgcga tccaagcatg   1140

tgaagttgat ggctactaca tccctaagga cgcgaggctt agcgtgaaca tttgggcgat   1200

cggtcgggac ccgaatgttt gggagaatcc gttggagttc ttgccggaaa gattcttgtc   1260

tgaagagaat gggaagatca atcccggtgg gaatgatttt aagctgattc cgtttggagc   1320

cggaggagga atttgtgcgg ggacaaggat gggaatggtc cttgtaagtt atattttggg   1380

cactttggtc cattcttttg attggaaatt accaaatggt gtcgctgagc ttaatatgga   1440

tgaaagtttt gggcttgcat tgcaaaaggc cgtgccgctc tcggccttgg tcagcccacg   1500

gttggcctca aacccgtacg caacctgagc taatgggctg ggcctagttt tgtgggccct   1560

aatttagaga cttttgtgtt ttaaggtgtg tactttatta attgggtgct aaaatgtgtg   1620

ttttaatttg tatttatggt taattatgac tttattgtat aattatttat ttttcccttc   1680

tgggtatttt atccatttaa tttttcttca gaattatgat catagttatc agaataaaat   1740

tgaaaataat gaatcggaaa aaaaaaaaaa aaaaaaaaaa aa                       1782
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<210> 12
<211> 506
<212> PRT
<213> viola

<400> 12

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Met Ala Ile Leu Val Thr Asp Phe Val Val Ala Ala Ile Ile Phe Leu
1               5                   10                  15
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- 16 -

Ile Thr Arg Phe Leu Val Arg Ser Leu Phe Lys Lys Pro Thr Arg Pro
            20   25   30

Leu Pro Pro Gly Pro Leu Gly Trp Pro Leu Val Gly Ala Leu Pro Leu
        35   40   45

Leu Gly Ala Met Pro His Val Ala Leu Ala Lys Leu Ala Lys Lys Tyr
    50   55   60

Gly Pro Ile Met His Leu Lys Met Gly Thr Cys Asp Met Val Val Ala
65   70   75   80

Ser Thr Pro Glu Ser Ala Arg Ala Phe Leu Lys Thr Leu Asp Leu Asn
            85   90   95

Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Ser His Leu Ala Tyr Gly
            100   105   110

Ala Gln Asp Leu Val Phe Ala Lys Tyr Gly Pro Arg Trp Lys Thr Leu
        115   120   125

Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Asp Asp
    130   135   140

Trp Ala Asn Val Arg Val Thr Glu Leu Gly His Met Leu Lys Ala Met
145   150   155   160

Cys Glu Ala Ser Arg Cys Gly Glu Pro Val Val Leu Ala Glu Met Leu
            165   170   175

Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val Ile Leu Ser Arg Arg
            180   185   190

Val Phe Val Thr Lys Gly Thr Glu Ser Asn Glu Phe Lys Asp Met Val
        195   200   205

Val Glu Leu Met Thr Ser Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile
    210   215   220

Pro Ser Ile Ala Trp Met Asp Leu Gln Gly Ile Glu Arg Gly Met Lys
225   230   235   240

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```
Lys Leu His Thr Lys Phe Asp Val Leu Leu Thr Lys Met Val Lys Glu
            245             250             255

His Arg Ala Thr Ser His Glu Arg Lys Gly Lys Ala Asp Phe Leu Asp
            260             265             270

Val Leu Leu Glu Glu Cys Asp Asn Thr Asn Gly Glu Lys Leu Ser Ile
            275             280             285

Thr Asn Ile Lys Ala Val Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
    290             295             300

Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu Thr Glu Met Ile Lys Asn
305             310             315             320

Pro Thr Ile Leu Lys Lys Ala Gln Glu Glu Met Asp Arg Val Ile Gly
            325             330             335

Arg Asp Arg Arg Leu Leu Glu Ser Asp Ile Ser Ser Leu Pro Tyr Leu
            340             345             350

Gln Ala Ile Ala Lys Glu Thr Tyr Arg Lys His Pro Ser Thr Pro Leu
            355             360             365

Asn Leu Pro Arg Ile Ala Ile Gln Ala Cys Glu Val Asp Gly Tyr Tyr
    370             375             380

Ile Pro Lys Asp Ala Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
385             390             395             400

Asp Pro Asn Val Trp Glu Asn Pro Leu Glu Phe Leu Pro Glu Arg Phe
            405             410             415

Leu Ser Glu Glu Asn Gly Lys Ile Asn Pro Gly Gly Asn Asp Phe Lys
            420             425             430

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met
            435             440             445

Gly Met Val Leu Val Ser Tyr Ile Leu Gly Thr Leu Val His Ser Phe
    450             455             460
```

```
Asp Trp Lys Leu Pro Asn Gly Val Ala Glu Leu Asn Met Asp Glu Ser
465             470             475             480


Phe Gly Leu Ala Leu Gln Lys Ala Val Pro Leu Ser Ala Leu Val Ser
                485             490             495


Pro Arg Leu Ala Ser Asn Pro Tyr Ala Thr
                500             505
```

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<211>  1659
<212>  DNA
<213>  salvia

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ggggccgagg ggctttctag tggtgggctc ccttcccttg ctgggcgaca tgccacatgt    180
cgccctagca aaaatggcca aaacttacgg cccgatcatg tacttgaaaa tgggcacagt    240
cggcatggtc gtggcgtcca cgccagacgc ggcgcgggcg ttcctaaaaa cccacgacgc    300
taatttctcg aaccggccgg tcaacgcggg tgccaccatc ctggcataca atgcccagga    360
catggtgttt gccccgtacg gccccaagtg gagactgctg aggaagctga gcagtctcca    420
catgctgggg agcaaggccc tggaggagtg ggctgacgtc cggacctcgg aggtggggca    480
catgctggcg gcgatgcacg aggccagccg cctgggcgag gccgtggggt tgccggagat    540
gctggtgtac gcgacggcga acatgatcgg gcaggtgata ttgagccgga gagttttcgt    600
gacgaaaggg aaggagatga atgaattcaa ggaaatggtg gtggagctca tgaccacagc    660
tggctatttc aacattggtg atttcattcc atggcttgct ggatggatt tgcaggggat    720
tgagagaggg atgaagaaac tgcacaagaa gtgggaccgc ttgatcggta agatgctgga    760
tgatcgattg aaatcaacct acaaacgcaa cgacaagcca gatcttcttg attctctctt    840
ggcaaatcat gatgatgaga gtaaggatga tgatgaggat tgcaagctca ccaccaccaa    900
tattaaagcc cttttactga atttatttac tgcagggaca gacacatcgt cgagcataat    960
agaatgggca ttagcagaca tgatcaagaa tccaagcatc caaaaaaggg ctcaccaaga   1020
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[illegible text]                                                    [illegible]
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cttcaaccct gacaggttta tgtcagggtt gcaggggatt gagcccggag ggaatcactt    1320

cgagctcatt ccctttgggg cggggcgcag gatctgcgcc ggcagcagaa tggggattgt    1380

aatagtggag tatttgctgg cgacactcgt gcactctttc gaatgggatt tgccggccgg    1440

ctcagcggag atggacatgg aggaggtgtt cgggctggcc ttgcagaaag ctgtaccact    1500

tgctgctagg ctcactccta ggttgccttc acattgctat gcacctcctt ctatttaatt    1560

tgcatattta catatgttgt gttacattga gcctttgcat atgttgtatc caacctatct    1620

tataacttgt gcatgaaatt gaaaaaaaaa aaaaaaaaa                           1659
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<210> 14
<211> 520
<212> PRT
<213> salvia

<400> 14

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1               5                   10                  15

Leu Val Val Ala Ser Leu Leu Tyr Ile Leu Ile Arg Met Phe Ile Ser
            20                  25                  30

Lys Leu Ser Thr Thr Gly His Pro Leu Pro Pro Gly Pro Arg Gly Phe
        35                  40                  45

Leu Val Val Gly Ser Leu Pro Leu Leu Gly Asp Met Pro His Val Ala
    50                  55                  60

Leu Ala Lys Met Ala Lys Thr Tyr Gly Pro Ile Met Tyr Leu Lys Met
65                  70                  75                  80

Gly Thr Val Gly Met Val Val Ala Ser Thr Pro Asp Ala Ala Arg Ala
                85                  90                  95

Phe Leu Lys Thr His Asp Ala Asn Phe Ser Asn Arg Pro Val Asn Ala
            100                 105                 110

Gly Ala Thr Ile Leu Ala Tyr Asn Ala Gln Asp Met Val Phe Ala Pro
        115                 120                 125
```

- 20 -

Tyr Gly Pro Lys Trp Arg Leu Leu Arg Lys Leu Ser Ser Leu His Met
130   135   140

Leu Gly Ser Lys Ala Leu Glu Glu Trp Ala Asp Val Arg Thr Ser Glu
145   150   155   160

Val Gly His Met Leu Ala Ala Met His Glu Ala Ser Arg Leu Gly Glu
                165   170   175

Ala Val Gly Leu Pro Glu Met Leu Val Tyr Ala Thr Ala Asn Met Ile
             180   185   190

Gly Gln Val Ile Leu Ser Arg Arg Val Phe Val Thr Lys Gly Lys Glu
        195   200   205

Met Asn Glu Phe Lys Glu Met Val Val Glu Leu Met Thr Thr Ala Gly
    210   215   220

Tyr Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ala Trp Met Asp Leu
225   230   235   240

Gln Gly Ile Glu Arg Gly Met Lys Lys Leu His Lys Lys Trp Asp Arg
            245   250   255

Leu Ile Gly Lys Met Leu Asp Asp Arg Leu Lys Ser Thr Tyr Lys Arg
            260   265   270

Asn Asp Lys Pro Asp Leu Leu Asp Ser Leu Leu Ala Asn His Asp Asp
        275   280   285

Glu Ser Lys Asp Asp Asp Glu Asp Cys Lys Leu Thr Thr Thr Asn Ile
    290   295   300

Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser
305   310   315   320

Ser Ile Ile Glu Trp Ala Leu Ala Glu Met Ile Lys Asn Pro Ser Ile
            325   330   335

Gln Lys Arg Ala His Gln Glu Met Asp Arg Val Ile Gly Arg Glu Arg
        340   345   350

- 21 -

```
Arg Leu Leu Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu Lys Ala Ile
        355             360.            365
```

```
Cys Lys Glu Ala Tyr Arg Lys His Pro Ser Thr Pro Leu. Asn Leu Pro
    370             375             380
```

```
Arg Ile Ser Thr Asp Ala Cys Val Val Asp Gly Tyr His Ile Pro Lys
385             390         .       395             400
```

```
Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Asp
            405             410             415
```

```
Val Trp Glu Asn Pro Leu Asp Phe Asn Pro Asp Arg Phe Met Ser Gly
  .       420             425             430
```

```
Leu Gln Gly Ile Glu Pro Gly Gly Asn His Phe Glu Leu Ile Pro Phe
        435             440             445
```

```
Gly Ala Gly Arg Arg Ile Cys Ala Gly Ser Arg Met Gly Ile Val Ile
    450     .       455             460
```

```
Val Glu Tyr Leu Leu Ala Thr Leu Val. His Ser Phe Glu Trp Asp Leu
465             470             475             480
```

```
Pro Ala Gly Ser Ala Glu Met Asp Met Glu Glu Val Phe Gly Leu Ala
            485         490             495
```

```
Leu Gln Lys Ala Val Pro Leu Ala Ala Arg Leu Thr Pro Arg Leu Pro
            500             505     .       510
```

```
Ser His Cys Tyr Ala Pro Pro Ser
            515             520
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<210>  15
<211>  1617
<212>  DNA
<213>  salvia

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ctctgccccc ggggccgagg ggctttccag tggtgggctc ccttccttg ctgggcgaca    180

tgccacatgt tgccctagca aaaatggcca aaacttatgg cccgatcatg tacttgaaaa    240
```

- 22 -

```
tgggcacagt cggcatggtc gtggcgtcca cgccagacgc ggcgcgggcg ttcctaaaaa   300

cccaggacgc taatttctct aaccggccgg tcaacgcggg tgccaccatc ctggcataca   360

atgcccagga catggtgttt gccccgtacg gccccaagtg gagattgctg aggaagctga   420

gcagtctcca catgctgggg agcaaggccc tggaggagtg ggccgacgtc cggacctcgg   480

aggtggggca catgctggcg gcgatgcacg aggccagccg cctggacgag gccgtggggt   540

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gagttttcgt gacgaaaggg aaggagatga atgagttcaa ggaaatggtg gtggagctca   660

tgaccacagc tggctatttc aacattggtg atttcattcc atggcttgct tggatggatt   720

tgcaggggat tgagagaggg atgaagaaac tgcacaagaa gtgggaccgc ttgatcggta   780

agatgctgga tgatcgattg aaatcaacct acaaacgcaa cgacaagcca gatcttcttg   840

attctctctt ggcaaatcat gatgatgaga gtaaggatga tgatgaggat tgcaagctca   900

ccaccaccaa tattaaagcc cttttactga atttatttac tgcagggaca gacacatcgt   960

cgagcataat agaatgggca ctagcggaga tgatcaagaa tccaagcatc caaaaaaggg   1020

ctcaccaaga gatggacaga gtcatcggga gagagcggcg tttgctcgaa tccgacatcc   1080

caaatctgcc atacctcaaa gccatatgca aagaggcata ccgaaaacac ccttccacgc   1140

cactaaacct gcctcggatc tccacggatg catgcgtcgt cgatggctac cacatcccca   1200

agaacacgag gttgagcgtc aacatctggg ccataggccg agatcccgac gtttgggaga   1260

atccccttga cttcaaccct gacaggttta tgtcagggtt gcaggggatt gagcccggag   1320

ggaatcactt cgagctcatt ccctttgggg cggggcgcag gatctgcgcc ggcagcagaa   1380

tggggattgt aatagtggag tatttgctgg cgacactcgt gcactctttc gaatgggatt   1440

tgccagccgg ctcagcggag atggacatgg aggaggtgtt cgggctggcc ttgcagaaag   1500

ctgtaccact tgctgctagg ctcactccta ggttgccttc acattgctat gcacctcctt   1560

ctatttaatt tgcatatttta tatatgttgt gttacattga aaaaaaaaa aaaaaaa     1617
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<210>   16
<211>   518
<212>   PRT
<213>   salvia

<400>   16

Met Glu Ala Gln Glu Asn Met Leu Leu Ile Ala Arg Ala Leu Val Val
1                5                   10                  15
```

- 23 -

Ala Ser Leu Leu Tyr Ile Leu Ile Arg Met Phe Ile Ser Lys Leu Ser
            20   25   30

Thr Pro Gly His Pro Leu Pro Pro Gly Pro Arg Gly Phe Pro Val Val
            35   40   45

Gly Ser Leu Pro Leu Leu Gly Asp Met Pro His Val Ala Leu Ala Lys
    50   55   60

Met Ala Lys Thr Tyr Gly Pro Ile Met Tyr Leu Lys Met Gly Thr Val
65   70   75   80

Gly Met Val Val Ala Ser Thr Pro Asp Ala Ala Arg Ala Phe Leu Lys
            85   90   95

Thr Gln Asp Ala Asn Phe Ser Asn Arg Pro Val Asn Ala Gly Ala Thr
            100   105   110

Ile Leu Ala Tyr Asn Ala Gln Asp Met Val Phe Ala Pro Tyr Gly Pro
            115   120   125

Lys Trp Arg Leu Leu Arg Lys Leu Ser Ser Leu His Met Leu Gly Ser
    130   135   140

Lys Ala Leu Glu Glu Trp Ala Asp Val Arg Thr Ser Glu Val Gly His
145   150   155   160

Met Leu Ala Ala Met His Glu Ala Ser Arg Leu Asp Glu Ala Val Gly
            165   170   175

Leu Pro Glu Met Leu Val Tyr Ala Thr Ala Asn Met Ile Gly Lys Val
            180   185   190

Ile Leu Ser Arg Arg Val Phe Val Thr Lys Gly Lys Glu Met Asn Glu
    195   200   205

Phe Lys Glu Met Val Val Glu Leu Met Thr Thr Ala Gly Tyr Phe Asn
    210   215   220

Ile Gly Asp Phe Ile Pro Trp Leu Ala Trp Met Asp Leu Gln Gly Ile
225   230   235   240

- 24 -

Glu Arg Gly Met Lys Lys Leu His Lys Lys Trp Asp Arg Leu Ile Gly
            245   250   255

Lys Met Leu Asp Asp Arg Leu Lys Ser Thr Tyr Lys Arg Asn Asp Lys
            260   265   270

Pro Asp Leu Leu Asp Ser Leu Leu Ala Asn His Asp Asp Glu Ser Lys
        275   280   285

Asp Asp Asp Glu Asp Cys Lys Leu Thr Thr Thr Asn Ile Lys Ala Leu
        290   295   300

Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile
305   310   315   320

Glu Trp Ala Leu Ala Glu Met Ile Lys Asn Pro Ser Ile Gln Lys Arg
                325   330   335

Ala His Gln Glu Met Asp Arg Val Ile Gly Arg Glu Arg Arg Leu Leu
            340   345   350

Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu Lys Ala Ile Cys Lys Glu
        355   360   365

Ala Tyr Arg Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Ile Ser
    370   375   380

Thr Asp Ala Cys Val Val Asp Gly Tyr His Ile Pro Lys Asn Thr Arg
385   390   395   400

Leu Ser Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Asp Val Trp Glu
                405   410   415

Asn Pro Leu Asp Phe Asn Pro Asp Arg Phe Met Ser Gly Leu Gln Gly
            420   425   430

Ile Glu Pro Gly Gly Asn His Phe Glu Leu Ile Pro Phe Gly Ala Gly
        435   440   445

Arg Arg Ile Cys Ala Gly Ser Arg Met Gly Ile Val Ile Val Glu Tyr
    450   455   460

```
Leu Leu Ala Thr Leu Val His Ser Phe Glu Trp Asp Leu Pro Ala Gly
465             470             475             480


Ser Ala Glu Met Asp Met Glu Glu Val Phe Gly Leu Ala Leu Gln Lys
            485             490             495


Ala Val Pro Leu Ala Ala Arg Leu Thr Pro Arg Leu Pro Ser His Cys
        500             505             510


Tyr Ala Pro Pro Ser Ile
        515
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<212>   DNA
<213>   sollya

<220>
<221>   misc_feature
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<223>   n = any nucleotide

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aagaccatgg cctattgtag gaaacctccc acaccttggc accaagccac accactccat     180
agctgccatg gctcggaaat acggtcccct cctgcacctc cgcatgggca tcgtgcacgt     240
ggtggttgcc gcctctgctg atgtggcggc acagttcttg aagaatgatg ccaacttctc     300
tagccggcca ccgaattctg gtgctaagca tatggcttat aactatcacg acatggtgtt     360
tgcaccctac ggtccaaggt ggcgcatgtt gaggaaaatt tgtgcccttc atatattctc     420
cgctaaggct ctcgatgatt ttcatcgcgt gcgtgaggag gaggttgcca tactcgcgag     480
gaccctagca cacgcaggcc aaaagccggt gaatttgggg cagttgttct ctacgtgtaa     540
tgctaatgcg ctatcagtgc tgatgctagg caggaggttg ttcagcacag aagttgattc     600
aaaagcatat gatttcaaac aaatggtggt ggagctgatg actctagccg gtgagtttaa     660
cgtcagtgat ttcatccac ccctcgagtg gctagacttg caaggcgtgg cagcgaaaat     720
gaagaacgtg cacaatcgat tcgatgcgtt tctgaatgta attttggagg agcataagct     780
gaaacttaat aatagtggac atggggaaca aaaacatatg gacttgttga gtacgttgat     840
tttgcttaag gatgatgctg atagtgaggg aggaaaactc actgatactg aaatcaaagc     900
```

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gctgcttttg aatttgtttt ctgctgggac ggacacttca tccagcacaa tagaatgggt    960
tatagctgag cttatacgca atcctaaaat cttagcccaa gcccaaagag agttggactt   1020
ggtggttggt ccaaatagac ttgtaacgga tttggacctc aaacaattaa cctacctaca   1080
agccatcgtc aaagaaacct ttcggctaca tcctgctacc ccactttcac ttccacggat   1140
cgcaaccgaa agctgtgaaa tcaacgggtt ttacattcca aagggctcaa cacttctcgt   1200
taacatatgg gccataggcc gtgatccaaa cacttgggct gaaccattgg tattccgacc   1260
tgaacgattc ttatcggatg gtgaaagtcc taatgttgat gttaaaggac gtaattttga   1320
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ggtccagtta gttactgcaa cgttaattca tgcatttaac tgggagttgc cagaagggga  ·1440
attgccagaa aatatgaata tggaggaaga ctatgggatt agcttgcaac ggacagtgcc   1500
attagttgtt catccaaagc caagactaga ccatgaagtt tatcagtccc atggagttgt   1560
aaactgagta cattcatgaa ctgacccaga agctgtcaga tgtcgtctta tattgcctta   1620
tgtagtgcga cccttgtgtg ttttttatgt attgttttgt acaaggttga agcccgtgcg   1680
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<210>  18
<211>  521
<212>  PRT
<213>  sollya

<400>  18

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1               5                  10                  15


Pro Phe Leu Tyr Cys Ile Leu Asn Met Arg Ile Leu Leu Asn Arg His
                20                  25                  30


Pro Arg Ser Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn
            35                  40                  45


Leu Pro His Leu Gly Thr Lys Pro His His Ser Ile Ala Ala Met Ala
        50                  55                  60


Arg Lys Tyr Gly Pro Leu Leu His Leu Arg Met Gly Ile Val His Val
65                  70                  75                  80
```

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```
Val Val Ala Ala Ser Ala Asp Val Ala Ala Gln Phe Leu Lys Asn Asp
            85              90                  95

Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala
            100             105             110

Tyr Asn Tyr His Asp Met Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg
            115             120             125

Met Leu Arg Lys Ile Cys Ala Leu His Ile Phe Ser Ala Lys Ala Leu
    130             135             140

Asp Asp Phe His Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ala Arg
145             150             155             160

Thr Leu Ala His Ala Gly Gln Lys Pro Val Asn Leu Gly Gln Leu Phe
            165             170             175

Ser Thr Cys Asn Ala Asn Ala Leu Ser Val Leu Met Leu Gly Arg Arg
            180             185             190

Leu Phe Ser Thr Glu Val Asp Ser Lys Ala Tyr Asp Phe Lys Gln Met
    195             200             205

Val Val Glu Leu Met Thr Leu Ala Gly Glu Phe Asn Val Ser Asp Phe
    210             215             220

Ile Pro Pro Leu Glu Trp Leu Asp Leu Gln Gly Val Ala Ala Lys Met
225             230             235             240

Lys Asn Val His Asn Arg Phe Asp Ala Phe Leu Asn Val Ile Leu Glu
            245             250             255

Glu His Lys Leu Lys Leu Asn Asn Ser Gly His Gly Glu Gln Lys His
            260             265             270

Met Asp Leu Leu Ser Thr Leu Ile Leu Leu Lys Asp Asp Ala Asp Ser
    275             280             285

Glu Gly Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn
    290             295             300
```

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Leu Phe Ser Ala Gly Thr Asp Thr Ser Ser Ser Thr Ile Glu Trp Val
305             310             315             320

Ile Ala Glu Leu Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Arg
                325             330             335

Glu Leu Asp Leu Val Val Gly Pro Asn Arg Leu Val Thr Asp Leu Asp
                340             345             350

Leu Lys Gln Leu Thr Tyr Leu Gln Ala Ile Val Lys Glu Thr Phe Arg
        355             360             365

Leu His Pro Ala Thr Pro Leu Ser Leu Pro Arg Ile Ala Thr Glu Ser
    370             375             380

Cys Glu Ile Asn Gly Phe Tyr Ile Pro Lys Gly Ser Thr Leu Leu Val
385             390             395             400

Asn Ile Trp Ala Ile Gly Arg Asp Pro Asn Thr Trp Ala Glu Pro Leu
            405             410             415

Val Phe Arg Pro Glu Arg Phe Leu Ser Asp Gly Glu Ser Pro Asn Val
            420             425             430

Asp Val Lys Gly Arg Asn Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg
        435             440             445

Arg Ile Cys Ala Gly Met Asn Phe Gly Leu Arg Met Val Gln Leu Val
    450             455             460

Thr Ala Thr Leu Ile His Ala Phe Asn Trp Glu Leu Pro Glu Gly Glu
465             470             475             480

Leu Pro Glu Asn Met Asn Met Glu Glu Asp Tyr Gly Ile Ser Leu Gln
            485             490             495

Arg Thr Val Pro Leu Val Val His Pro Lys Pro Arg Leu Asp His Glu
            500             505             510

Val Tyr Gln Ser His Gly Val Val Asn
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aaaaggttgg ccaattgtgg gtgcactgcc tctaatggga agcatgcccc atgtcacact   180

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ctccaatcgc cccccaaatg ctggggcaac tcacttagct tatgatgccc aggacatggt   360

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tgattttatt ccctttttgg ctcgcttcga cctccaaggc atcgagcgtg gcatgaaaac   780

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gcacccatca acgccactca acttgcctag aatctcatcc caagcatgcc aagtgaatgg   1200

ctactacatc ccaaagaaca ctaggcttag tgtcaacatc tgggccattg gaagagaccc   1260

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Thr His Leu Val Ile Arg Leu Val Leu Lys Glu Lys Glu Gln Arg Lys
            20                  25                  30


Leu Pro Pro Gly Pro Lys Gly Trp Pro Ile Val Gly Ala Leu Pro Leu
        35                  40                  45


Met Gly Ser Met Pro His Val Thr Leu Ser Glu Met Ala Lys Lys Tyr
        50                  55                  60


Gly Pro Val Met Tyr Leu Lys Met Gly Thr Asn Asn Met Ala Val Ala
65                  70                  75                  80


Ser Thr Pro Ser Ala Ala Arg Ala Phe Leu Lys Thr Leu Asp Leu Asn
                85                  90                  95


Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr His Leu Ala Tyr Asp
                100                 105                 110


Ala Gln Asp Met Val Phe Ala Asp Tyr Gly Ser Arg Trp Lys Leu Leu
        115                 120                 125
```

Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly Lys Ala Leu Glu Glu
    130   135   140

Trp Ser Gln Val Arg Glu Ile Glu Met Gly His Met Leu Arg Ala Met
145   150   155   160

Tyr Asp Cys Ser Gly Gly Gly Asp Gly Asn Asn Asp Asn Asp Gly Asn
              165   170   175

Lys Lys Lys Gly Thr Arg His Glu Pro Ile Val Val Ala Glu Met Leu
            180   185   190

Thr Tyr Ala Met Ala Asn Met Ile Gly Pro Ser Asp Leu Glu Pro Ser
        195   200   205

Cys Ile Pro Arg Gln Arg Val Arg Asn Arg Thr Ser Leu Arg Thr Trp
    210   215   220

Trp Phe Lys Leu Met Thr Val Ala Gly Tyr Phe Asn Ile Gly Asp Phe
225   230   235   240

Phe Pro Phe Leu Ala Arg Arg Arg Arg Gln Gly Ile Glu Arg Gly Met
              245   250   255

Lys Thr Leu His Asn Lys Lys Asp Asp Leu Leu Thr Thr Met Ile His
            260   265   270

Glu His Val Ala Ser Ala His Lys Arg Lys Gly Lys Pro Pro Phe Leu
        275   280   285

Asp Val Leu Met Ala His His Thr Asn Glu Ser His Glu Leu Ser Leu
    290   295   300

Thr Asn Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp
305   310   315   320

Thr Ser Ser Ser Ile Ile Glu Trp Ala Leu Ala Glu Met Leu Ile Asn
              325   330   335

Pro Lys Ile Met Lys Lys Val His Glu Glu Met Asp Lys Val Ile Gly
            340   345   350

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```
Lys Asp Arg Arg Leu Lys Glu Ser Asp Ile Glu Asn Leu Pro Tyr Leu
        355             360             365

Gln Ala Ile Cys Lys Glu Thr Tyr Arg Lys His Pro Ser Thr Pro Leu
    370             375             380

Asn Leu Pro Arg Ile Ser Ser Gln Ala Cys Gln Val Asn Gly Tyr Tyr
385             390             395             400

Ile Pro Lys Asn Thr Arg Leu Ser Val Asn Ile Trp Ala Ile Gly Arg
            405             410             415

Asp Pro Asn Val Trp Glu Asn Pro Leu Glu Phe Asn Pro Glu Arg Phe
            420             425             430

Met Gly Ala Asn Lys Thr Ile Asp Pro Arg Gly Asn Asp Phe Glu Leu
        435             440             445

Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Thr Arg Met Gly
    450             455             460

Ile Val Leu Val Gln Tyr Ile Leu Gly Thr Leu Val His Ser Phe Asp
465             470             475             480

Trp Lys Leu Pro Asn Gly Val Val Glu Leu Asn Met Glu Glu Thr Phe
            485             490             495

Gly Leu Ala Leu Gln Lys Lys Ile Pro Leu Ser Ala Leu Ile Thr Pro
        500             505             510

Arg Leu Pro Pro Thr Ala Tyr Asn Val Ile Asn Ser Ser
    515             520             525
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gccgccttcc accagggccc accggatggc caatcctagg tgcccttcct cttttgggca       180

acatgccaca tgttactttt gctaacatgg cgaaaaaata tggctcggta atgtacctaa       240
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<213>    gentiana
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- 34 -

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1   5   10   15

Phe Leu Phe Phe His Val Gln Lys Leu Val His Tyr Leu His Gly Lys
            20   25   30

Ala Thr Gly His Arg Cys Arg Arg Leu Pro Pro Gly Pro Thr Gly Trp
        35   40   45

Pro Ile Leu Gly Ala Leu Pro Leu Leu Gly Asn Met Pro His Val Thr
    50   55   60

Phe Ala Asn Met Ala Lys Lys Tyr Gly Ser Val Met Tyr Leu Lys Val
65   70   75   80

Gly Ser His Gly Leu Ala Ile Ala Ser Thr Pro Asp Ala Ala Lys Ala
                85   90   95

Phe Leu Lys Thr Leu Asp Leu Asn Phe Ser Asn Arg Pro Pro Asn Ala
            100   105   110

Gly Ala Thr His Leu Ala Tyr Asn Ala Gln Asp Met Val Phe Ala His
        115   120   125

Tyr Gly Pro Lys Trp Lys Leu Leu Arg Lys Leu Ser Asn Leu His Met
    130   135   140

Leu Gly Gly Lys Ala Leu Glu Asn Trp Ala Asp Val Arg Lys Thr Glu
145   150   155   160

Leu Gly Tyr Met Leu Lys Ala Met Phe Glu Ser Ser Gln Asn Asn Glu
                165   170   175

Pro Val Met Ile Ser Glu Met Leu Thr Tyr Ala Met Ala Asn Met Leu
            180   185   190

Ser Gln Val Ile Leu Ser Arg Arg Val Phe Asn Lys Lys Gly Ala Lys
        195   200   205

Ser Asn Glu Phe Lys Asp Met Val Val Glu Leu Met Thr Ser Ala Gly
    210   215   220

Tyr Phe Asn Ile Gly Asp Phe Ile Pro Ser Ile Gly Trp Met Asp Leu
225   230   235   240

Gln Gly Ile Glu Gly Gly Met Lys Arg Leu His Lys Lys Phe Asp Val
                245   250   255

Leu Leu Thr Arg Leu Leu Asp Asp His Lys Arg Thr Ser Gln Glu Arg
            260   265   270

Lys Gln Lys Pro Asp Phe Leu Asp Phe Val Ile Ala Asn Gly Asp Asn
        275   280   285

Ser Asp Gly Glu Arg Leu Asn Thr Asp Asn Ile Lys Ala Leu Leu Leu
    290   295   300

Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile Glu Trp
305   310   315   320

Ala Leu Ala Glu Leu Leu Lys Asn Arg Thr Leu Leu Thr Arg Ala Gln
            325   330   335

Asp Glu Met Asp Arg Val Ile Gly Arg Asp Arg Arg Leu Leu Glu Ser
            340   345   350

Asp Ile Pro Asn Leu Pro Tyr Leu Gln Ala Ile Cys Lys Glu Thr Phe
        355   360   365

Arg Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Asn Cys Ile Arg
    370   375   380

Gly His Val Asp Val Asn Gly Tyr Tyr Ile Pro Lys Gly Thr Arg Leu
385   390   395   400

Asn Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Ser Val Trp Gly Asp
            405   410   415

Asn Pro Asn Glu Phe Asp Pro Glu Arg Phe Leu Tyr Gly Arg Asn Ala
        420   425   430

Lys Ile Asp Pro Arg Gly Asn His Phe Glu Leu Ile Pro Phe Gly Ala
        435   440   445

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Gly Arg Arg Ile Cys Ala Gly Thr Arg Met Gly Ile Leu Leu Val Glu
    450                 455             460


Tyr Ile Leu Gly Thr Leu Val His Ser Phe Asp Trp Lys Leu Gly Phe
465                 470             475                 480


Ser Glu Asp Glu Leu Asn Met Asp Glu Thr Phe Gly Leu Ala Leu Gln
                485             490                 495


Lys Ala Val Pro Leu Ala Ala Met Val Ile Pro Arg Leu Pro Leu His
                500             505             510


Val Tyr Ala Pro
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cacggaaaag aagttcattg aacaataatg gatataaaaa ttgcggtcaa cacattggtg   900

agggaaatat ttttatcagc acaccaacat ttccaaacat caataaagca atgaagatgg   960
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aaaaagcaag ataaaaatag tatatggaag aaaaatacaa atgcttatat gacagaagtc   1980

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- 38 -

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aggtagaata tgataattta ttcttttaca tataacaatg aaataaataa gaataattag     3360

gtaaaatata tgtatagtag atacatgttt ttctcaatgg gcataaaaat gtgaaattca     3420

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cgaatgcgag tatttaacct gagtttggta attatgtacc atcagaaatc gcatcgaatg     3540

taactcaaaa atagtacaaa caaattccct cactgctcca ttggccatta atttaggtcc     3600

aattttcact ctataaaagc ccataggatc tctctagctt ttgtactcaa cactcaggca     3660

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cgagtgtgat agagtgggca ctagcggaga tgttgaaaaa tccccacata acaaagagag   1140

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agaacactag gctgagtgtg aacatatggg ccattggaag agaccccgag gtgtgggaga   1380

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atgggaatga ttttgagctg attccgtttg gtgctgggag aagggtgtgt gctgggacaa   1500

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agctaccaaa tggggtggtg gagttgaaca tggaagagac ctttgggctt gccttgcaga   1620

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agagttgggt ttggtttggt tcaccaactc tgttcaaaca ttatgtctag ctatttaaaa   1740

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<213> kennedia

<400> 27

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Ile Leu Ile Phe Leu Ile Thr His Leu Thr Ile His Ser Leu Phe Thr
            20   25   30

Asn Arg His Lys Lys Leu Pro Pro Gly Pro Arg Gly Trp Pro Ile Val
        35   40   45

Gly Ala Leu Pro Val Leu Gly Ser Met Pro His Val Thr Leu Ser Arg
    50   55   60

Met Ala Lys Lys Tyr Gly Pro Val Met Tyr Leu Lys Met Gly Thr Lys
65   70   75   80

Asn Met Val Val Ala Ser Thr Pro Ala Ala Ala Arg Ala Phe Leu Lys
                85   90   95

Thr Leu Asp Gln Asn Phe Ser Asn Arg Pro Pro Asn Ala Gly Ala Thr
            100   105   110

His Leu Ala Tyr Asp Ser Gln Asp Met Val Phe Ala His Tyr Gly Ser
            115   120   125

Arg Trp Arg Leu Leu Arg Lys Leu Ser Asn Leu His Met Leu Gly Gly
    130   135   140

Lys Ala Leu Asp Asp Trp Ala His Val Arg Glu Lys Glu Met Arg Tyr
145   150   155   160

Met Leu Gly Ser Met Tyr Asp Cys Ser Lys Arg Gly Glu Ala Val Val
                165   170   175

Val Ala Glu Met Leu Thr Tyr Ala Met Ala Asn Met Ile Gly Gln Val
            180   185   190

Ile Leu Ser Arg Arg Val Phe Glu Ser Lys Gly Ser Glu Ser Asn Glu
        195   200   205

Phe Lys Asp Met Val Val Glu Leu Met Thr Val Ala Gly Tyr Phe Asn
    210   215   220

Ile Gly Asp Phe Val Pro Phe Leu Ala Trp Phe Asp Leu Gln Gly Ile
225   230   235   240

Glu Arg Glu Met Lys Ala Leu His Lys Lys Phe Asp Ala Leu Leu Thr
            245   250   255

Arg Met Ile Glu Glu His Val Ala Ser Arg Cys His Lys Gly Lys Gly
        260   265   270

Asn Tyr Asp Phe Leu Asp Val Val Met Asp His Ser Ser Glu Ser Ser
    275   280   285

Asp Gly Glu Arg Leu Thr Leu Thr Asn Val Lys Ala Leu Leu Leu Asn
    290   295   300

Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Val Ile Glu Trp Ala
305   310   315   320

Leu Ala Glu Met Leu Lys Asn Pro His Ile Thr Lys Arg Ala His Glu
            325   330   335

Glu Met Asp Gln Val Ile Gly Lys Asp Arg Arg Leu Lys Glu Ser Asp
            340   345   350

Leu Arg Asn Leu Pro Tyr Leu Gln Ala Ile Cys Lys Glu Ala Leu Arg
        355   360   365

Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Val Ser Ser Gln Pro
    370   375   380

Cys Gln Val Asn Gly Tyr Tyr Ile Pro Lys Asn Thr Arg Leu Ser Val
385   390   395   400

Asn Ile Trp Ala Ile Gly Arg Asp Pro Glu Val Trp Glu Asn Pro Cys
                405   410   415

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Glu Phe Asn Pro Glu Arg Phe Met Ser Gly Lys Gly Ala Lys Val Asp
            420             425             430

Pro His Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg
        435             440             445

Val Cys Ala Gly Thr Arg Met Gly Ile Val Met Val Gln Tyr Ile Leu
    450             455             460

Gly Thr Leu Val His Ser Phe Glu Trp Lys Leu Pro Asn Gly Val Val
465             470             475             480

Glu Leu Asn Met Glu Glu Thr Phe Gly Leu Ala Leu Gln Lys Lys Val
            485             490             495

Pro Leu Ser Ala Leu Val Ser Pro Arg Leu His Pro Ser Ser Tyr Ile
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Gln
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atcccgatta ctattttcgg atcactaaaa gtgaacacat ggtggatctt aaagagaaat   240

tcaagcgcat gtgcgacaag tctatgataa gaaaacgata catgcacctc acggaggagt   300

atcttaaaga gaacccaaac ctttgtgagt acatggctcc gtccctcgat gctcgccagg   360

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aatggggaca accaaaatct aaaatcaccc acctaatctt ctgcaccaca tctggtgtag   480

atatgcccgg ggctgattac caactcacca aactcctcgg cctccgccct tcggtcaaac   540

gttttatgat gtaccaacaa gggtgctttg caggtgggac ggttcttcgt ctagcaaaag   600

acctcgcaga aaacaacaag gatgcacgtg tcctagttgt ttgttccgag attactgcag   660

tcacattccg tggtcctaac gacactcatc ttgattcact cgttggtcaa gctttgtttg   720
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gggatggagc tgcggctgtc attgttggtt cagaccctga cttgacaaaa gagcgtccat    780

tgttcgagat gatatctgct gctcaaacta tcttaccaga ctcggaggga gcaatcgatg    840

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ccaagaacat agagaaggca ttgacacaag ccttttctcc attaggtata agtgactgga    960

actcgatctt ttggatcgct catcctggtg gtccagctat tctggaccaa gttgagctta   1020

agctcggtct caaggaggag aagatgagag ccactagaca cgttcttagt gagtatggaa   1080

acatgtcaag tgcttgtgtt ttgttcatta tggatgaaat gaggaagaaa tcggctgagg   1140

aaggtgcagc cacaaccggt gaagggctag attggggtgt tttattcggg ttcggtcctg   1200

gtttgacggt cgaaccgtg  gtcctccaca gcctccaac  cactgtatcg gttgcaaatt   1260

aatttagttg catggttatg gatataagcg tcttttgttg gaacaattaa attttttactg   1320

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<211> 398
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<400> 29

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Gln Gly Pro Ala Thr Ile Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
            20                  25                  30


Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Arg Ile Thr Lys
        35                  40                  45


Ser Glu His Met Val Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
    50                  55                  60


Lys Ser Met Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Tyr Leu
65                  70                  75                  80


Lys Glu Asn Pro Asn Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala
                85                  90                  95


Arg Gln Asp Val Val Val Val Glu Val Pro Lys Leu Gly Lys Glu Ala
                100                 105                 110
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- 44 -

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Ala Thr Lys Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr
        115             120             125

His Leu Ile Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
    130             135             140

Tyr Gln Leu Thr Lys Leu Leu Gly Leu Arg Pro Ser Val Lys Arg Phe
145             150             155             160

Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
            165             170             175

Ala Lys Asp Leu Ala Glu Asn Asn Lys Asp Ala Arg Val Leu Val Val
            180             185             190

Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro Asn Asp Thr His
    195             200             205

Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
    210             215             220

Val Ile Val Gly Ser Asp Pro Asp Leu Thr Lys Glu Arg Pro Leu Phe
225             230             235             240

Glu Met Ile Ser Ala Ala Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
            245             250             255

Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
            260             265             270

Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Lys Ala Leu Thr Gln
        275             280             285

Ala Phe Ser Pro Leu Gly Ile Ser Asp Trp Asn Ser Ile Phe Trp Ile
    290             295             300

Ala His Pro Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Leu Lys Leu
305             310             315             320

Gly Leu Lys Glu Glu Lys Met Arg Ala Thr Arg His Val Leu Ser Glu
            325             330             335
```

- 45 -

Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
            340   345   350

Arg Lys Lys Ser Ala Glu Glu Gly Ala Ala Thr Thr Gly Glu Gly Leu
        355   360   365

Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
    370   375   380

Val Val Leu His Ser Leu Pro Thr Thr Val Ser Val Ala Asn
385   390   395

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ggccatgatt acttagtacc acatgtaact gagacttgca atggacaagt acttattatc   180
ctacaaccta acttctttgt tgtgtttaag tccaaaaagt tatgcgtgcg gccagaatcc   240
atcaaaatgt gtagcatttg tttcaacaca tgcccttttaa cccgtatagt gttatgagtt   300
ggtactccag acaatacatt aagagatata ttgggtatgc attgttgtgt atcatctccc   360
acacatgctc agttatgtca gtatcacaat cttcctcttc caaacacaat tctaattctc   420
cttccttctc atctctaatc tctaaagtaa acatttgacc ttcacactta tgaccatgca   480
tatacttctt atcacgataa aaacatagat tcttagccct cttttcagca tacttttttt   540
tacttaatta ctttctaggt gtaggcatgg tgtttgcaaa ctgtttggtt accaactgag   600
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acattccaat tattattgta cttaggagta ggcaacaatg agacacttt tttcttaaca   720
actgctagcc tagcttcttc catcttagcc caacaataga catcatttaa actagttggt   780
ttaaacatgc taaccagcat aactatttcg tctttcaatc caccaatata caaactaata   840

- 46 -

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gcatgagatt cactcaattc caccttattc aataaaactt caaaagaatc ttggtatacc   900

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tcaaaccttt tcttgatatg cctttcatac atatcccgag taacaatttc cccatgtctt  1020

tttcataaat tgcttgtttt agttaagggc tttgtcaaac acatgcatag agacaagcct  1080

gatcctaatg aatgaagaac attaacaaaa tcactaaaag aatcaagaac actaacataa  1140

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acaattccta aggctaagta gggttggatc agttggaaaa ccccttgcct ctcaaccgag  1260

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ccacatcagc tttatctctc caatgacccg atgacgacca agttgccaca gtcggtgacc  1560

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agatcaagaa ttgacagtgt accggaaaat gtaacaagat aactgaatta taacataatg  1920

gagttattag ttgtgatcaa atagcatgat gatgctctat tacccattga aatgtactaa  1980

atgtaatgac ttaaccataa tccataagat tgaaagttaa cataatcaaa cacaagaatt  2040

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gtttgtcaca aagacttaag agagagcaaa tcatccaaaa actgattacc aaatgaagaa  2160

atgaaaatat ttaaagagaa ttacaaatgg cttgaaaatc ggttatgtgg tttgtttgaa  2220

cttttgaagc tgtcacgtga tataacacat aatatatctt tatctttgtg atgcaccatg  2280

tatgatacaa ctaataagtt gtatcaatat caatttctta aaaactggat atacttttc   2340

ggtaacttat ttaagtccaa tgtattattt agtccctatg aaaagcgtct caatgatatt  2400

tccccaagtc aaatgttaga ttttttattt tatttatttt taaattcagc cataggcaaa  2460

aatattagta agtcagctta tgcgtcccaa atataattgt tatacggctt aaatgatttg  2520

caattactac attttttatgt aatcatatct caatcaacag aattatgaga tgtggttgta  2580
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- 47 -

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acagatatcg aagctcaatt gtgtaatgtt tttcaatggt ccacaacgtg gcatctatga   2820

ccatcgttcg taaaacttgg gtacgtcata cctaccacac gttccctcta tataagaaac   2880

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aaacttacgg ccccatcatc tacctaaaag tcggtgcatg gggcatggcc gtcgcgtcaa    300

cgcctgcctc cgcccgtgcg tttctcaaaa ccctagacac caacttctct gaccgccctc    360

cgaatgcggg tgccaccata ttagcctaca acgcggaaga tatggtgttc gcccgctatg    420

gcccaaagtg gagattgctc agaaaactga caatctcca catgttgggg aatcatgctt     480

tagatgggtg ggcaagtgta aggtcctccg agttgggcta catgctccat gcaaggcacg    540

acgccaccg tcatggcgag cccgtggtgc tgccagagat gctcatgtac gccgtgggga     600

atatgctcgg gcaggtgata ttaagtagac ggattttcga gaagaaggg aaggaggtga     660

atgagttgaa agatatggtg gtggagctca tgacttcagc tggatatttc aatattggtg    720

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tgcacaataa gttcgacaag ttgatcggca aaatgattga ggatcatttg aaatcagccc    840

acatacgcaa ggccaagccg gatcttcttg attgcctctt ggcaaatcgt gatagctccg    900

atgcggagaa gctcacctca accaacgtca aggcccttttt actgaacttg ttcaccgcag    960

ggaccgacac gtcatcaagc ataatagaat gggcattggc cgagatgatc aagaatccaa   1020

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- 48 -

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tcgaatcgga catcccgaac ctaccctacc tacgagccat atgtaaagaa acatatcgca   1140

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ggtattacat acctaaaaac acccggctca gcgttaacat atgggctatc gggagagacc   1260

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agcggattga tccccgcggg aaccacttcg agctcatccc gttcggggct gggcggagga   1380

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<213> lavendula

<400> 32

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Ala Ala Ser Ile Tyr Phe Leu Ile Arg Tyr Phe Leu Ser Arg Ile Ile
            20   25   30

Thr Thr Ile Thr His Gly Gly Ser His Arg Leu Pro Pro Gly Pro Arg
        35   40   45

Gly Phe Pro Ile Val Gly Ala Leu Pro Leu Leu Gly Asp Met Pro His
    50   55   60

Val Ala Leu Ala Lys Met Ala Lys Thr Tyr Gly Pro Ile Ile Tyr Leu
65   70   75   80

Lys Val Gly Ala Trp Gly Met Ala Val Ala Ser Thr Pro Ala Ser Ala
                85   90   95
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Arg Ala Phe Leu Lys Thr Leu Asp Thr Asn Phe Ser Asp Arg Pro Pro
        100              105              110

Asn Ala Gly Ala Thr Ile Leu Ala Tyr Asn Ala Glu Asp Met Val Phe
        115              120              125

Ala Arg Tyr Gly Pro Lys Trp Arg Leu Leu Arg Lys Leu Thr Asn Leu
    130              135              140

His Met Leu Gly Asn His Ala Leu Asp Gly Trp Ala Ser Val Arg Ser
145              150              155              160

Ser Glu Leu Gly Tyr Met Leu His Ala Arg His Asp Ala Thr Arg His
                165              170              175

Gly Glu Pro Val Val Leu Pro Glu Met Leu Met Tyr Ala Val Gly Asn
            180              185              190

Met Leu Gly Gln Val Ile Leu Ser Arg Arg Ile Phe Glu Lys Lys Gly
        195              200              205

Lys Glu Val Asn Glu Leu Lys Asp Met Val Val Glu Leu Met Thr Ser
210              215              220

Ala Gly Tyr Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ala Trp Met
225              230              235              240

Asp Leu Gln Gly Ile Glu Ser Gly Met Lys Lys Leu His Asn Lys Phe
            245              250              255

Asp Lys Leu Ile Gly Lys Met Ile Glu Asp His Leu Lys Ser Ala His
        260              265              270

Ile Arg Lys Ala Lys Pro Asp Leu Leu Asp Cys Leu Leu Ala Asn Arg
    275              280              285

Asp Ser Ser Asp Ala Glu Lys Leu Thr Ser Thr Asn Val Lys Ala Leu
290              295              300

Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Ile Ile
305              310              315              320

Glu Trp Ala Leu Ala Glu Met Ile Lys Asn Pro Thr Ile Leu Asn Arg
```

- 50 -

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                    325                    330                    335

Ala His Gln Glu Met Asp Arg Val Val Gly Arg Thr Arg Arg Leu Val
            340             345             350

Glu Ser Asp Ile Pro Asn Leu Pro Tyr Leu Arg Ala Ile Cys Lys Glu
            355             360             365

Thr Tyr Arg Lys His Pro Ser Thr Pro Leu Asn Leu Pro Arg Ile Ala
    370             375             380

Ser Glu Pro Cys Val Val Asp Gly Tyr Tyr Ile Pro Lys Asn Thr Arg
385             390             395             400

Leu Ser Val Asn Ile Trp Ala Ile Gly Arg Asp Pro Asp Val Trp Glu
            405             410             415

Asn Pro Leu Asp Phe Asn Pro Asp Arg Phe Leu Ser Gly Lys Asn Glu
            420             425             430

Arg Ile Asp Pro Arg Gly Asn His Phe Glu Leu Ile Pro Phe Gly Ala
            435             440             445

Gly Arg Arg Ile Cys Ala Gly Ala Arg Met Gly Met Val Leu Val Glu
    450             455             460

Tyr Ile Leu Gly Thr Leu Val His Ala Phe Glu Trp Glu Leu Pro Ala
465             470             475             480

Gly Ala Gly Ala Gly Thr Ala Glu Leu Asn Met Asp His Val Phe Gly
            485             490             495

Leu Ala Leu Gln Lys Ala Val Pro Leu Thr Ala Met Leu Thr Pro Arg
            500             505             510

Leu Pro Ser His Cys Tyr Ala Pro
            515             520
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